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TECH CENTER 1600/2900

PH-15

1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/591,447D

DATE: 04/29/2002
TIME: 16:41:15

Input Set : A:\KCO1003textfile.txt
Output Set: N:\CRF3\04292002\I591447D.raw

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MAY 0 7 2002

TECH CENTER 1600/2900

```
 3 <110> APPLICANT: Chatfield, Steven N
 4        Dougan, Gordon
 5        Sydenham, Mark
 7 <120> TITLE OF INVENTION: Vaccines Containing Attenuated Bacteria
 9 <130> FILE REFERENCE: KCO1003US
11 <140> CURRENT APPLICATION NUMBER: US 09/591,447D
12 <141> CURRENT FILING DATE: 2001-06-09
14 <150> PRIOR APPLICATION NUMBER: UK 9726233.1
15 <151> PRIOR FILING DATE: 1997-12-11
17 <160> NUMBER OF SEQ ID NOS: 4
19 <170> SOFTWARE: MS-DOS
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1287
23 <212> TYPE: DNA
24 <213> ORGANISM: Salmonella typhimurium
26 <400> SEQUENCE: 1
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32 gacgttgatg gcttaatgca atcagtcaaa ctcaacgcgg gtcaggcagg tcagcagctt     180
34 ccggacgacg ccacgctgcg tcaccagatc ctggaacgtt tgattatgga tcaaattatc     240
36 ctgcagatgg gtcagaagat gggggtgaag atcacggatg agcagttgga tcagccatca     300
38 gccaacatcg ccaaacaaaa caatatgacg atggatcaga tgcgcagccg tctggcttac     360
40 gatgggctga actattcaac ctaccgtaac cagattcgta aagagatgat tatctctgaa     420
42 gtgcgcaaca atgaggttcg tcgccgtatc accgttttgc cgcaagaagt tgacgcgctg     480
44 gcaaaacaga ttggcaccca aaacgatgcc agcaccgagc tgaacctgag ccatatcctg     540
46 attgctctgc cggaaaaccc aacctccgag caggttaacg acgcgcagcg ccaggcggaa     600
48 agcattgttg aagaagcgcg taacggcgca gatttcggca aactggcgat tacctactct     660
50 gccgaccagc aggcgctaaa aggcggtcag atgggctggg ccgtatcca ggagctgccg      720
52 gggattttcg cccaggcgct gagcaccgcg aagaaaggcg acattgtcgg cccgattcgc     780
54 tccggcgtcg gcttccacat tctgaaagta aatgacctgc gcggtcagag ccagagtatc     840
56 tccgtgaccg aagttcacgc tcgtcacatt ctgcttaagc cgtcgccgat catgaacgat     900
58 cagcaggcgc gcctgaagct ggaagaaatc gcggctgaca ttaagagtgg taaaaccacc     960
60 tttgccgctg cggcgaaaga gtactctcag gacccgggct ccgctaacca gggcggtgat    1020
62 ttgggttggg ctacgccaga tattttcgac ccggcgttcc gcgacgcgct aacgaagctg    1080
64 cataaaggcc aaataagcgc gccggtacac tcctctttcg gctggcatct gatcgaattg    1140
66 ctggatacgc gtaaggtaga caaaaccgat gcggcgcaga agatcgcgc ttatcgtatg     1200
68 ctgatgaacc gtaaattctc agaagaagcg gcgacctgga tgcaagaaca gcgcgccact    1260
70 tacgttaaga ttttgagtaa ctaatga                                        1287
73 <210> SEQ ID NO: 2
74 <211> LENGTH: 427
75 <212> TYPE: PRT
76 <213> ORGANISM: Salmonella typhimurium
78 <400> SEQUENCE: 2
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80  Met Lys Asn Trp Lys Thr Leu Leu Leu Gly Ile Ala Met Ile Ala Asn
81   1               5               10              15
83  Thr Ser Phe Ala Ala Pro Gln Val Val Asp Lys Val Ala Ala Val Val
84               20              25              30
86  Asn Asn Gly Val Val Leu Glu Ser Asp Val Asp Gly Leu Met Gln Ser
87           35              40              45
89  Val Lys Leu Asn Ala Gly Gln Ala Gly Gln Gln Leu Pro Asp Asp Ala
90       50              55              60
92  Thr Leu Arg His Gln Ile Leu Glu Arg Leu Ile Met Asp Gln Ile Ile
93   65              70              75              80
95  Leu Gln Met Gly Gln Lys Met Gly Val Lys Ile Thr Asp Glu Gln Leu
96               85              90              95
98  Asp Gln Pro Ser Ala Asn Ile Ala Lys Gln Asn Asn Met Thr Met Asp
99               100             105             110
101 Gln Met Arg Ser Arg Leu Ala Tyr Asp Gly Leu Asn Tyr Ser Thr Tyr
102         115             120             125
104 Arg Asn Gln Ile Arg Lys Glu Met Ile Ile Ser Glu Val Arg Asn Asn
105     130             135             140
107 Glu Val Arg Arg Arg Ile Thr Val Leu Pro Gln Glu Val Asp Ala Leu
108 145             150             155             160
110 Ala Lys Gln Ile Gly Thr Gln Asn Asp Ala Ser Thr Glu Leu Asn Leu
111             165             170             175
113 Ser His Ile Leu Ile Ala Leu Pro Glu Asn Pro Thr Ser Glu Gln Val
114             180             185             190
116 Asn Asp Ala Gln Arg Gln Ala Glu Ser Ile Val Glu Glu Ala Arg Asn
117         195             200             205
119 Gly Ala Asp Phe Gly Lys Leu Ala Ile Thr Tyr Ser Ala Asp Gln Gln
120     210             215             220
122 Ala Leu Lys Gly Gly Gln Met Gly Trp Gly Arg Ile Gln Glu Leu Pro
123 225             230             235             240
125 Gly Ile Phe Ala Gln Ala Leu Ser Thr Ala Lys Lys Gly Asp Ile Val
126             245             250             255
128 Gly Pro Ile Arg Ser Gly Val Gly Phe His Ile Leu Lys Val Asn Asp
129             260             265             270
131 Leu Arg Gly Gln Ser Gln Ser Ile Ser Val Thr Glu Val His Ala Arg
132     275             280             285
134 His Ile Leu Leu Lys Pro Ser Pro Ile Met Asn Asp Gln Gln Ala Arg
135     290             295             300
137 Leu Lys Leu Glu Glu Ile Ala Ala Asp Ile Lys Ser Gly Lys Thr Thr
138 305             310             315             320
140 Phe Ala Ala Ala Ala Lys Glu Tyr Ser Gln Asp Pro Gly Ser Ala Asn
141             325             330             335
143 Gln Gly Gly Asp Leu Gly Trp Ala Thr Pro Asp Ile Phe Asp Pro Ala
144             340             345             350
146 Phe Arg Asp Ala Leu Thr Lys Leu His Lys Gly Gln Ile Ser Ala Pro
147     355             360             365
149 Val His Ser Ser Phe Gly Trp His Leu Ile Glu Leu Leu Asp Thr Arg
150     370             375             380
152 Lys Val Asp Lys Thr Asp Ala Ala Gln Lys Asp Arg Ala Tyr Arg Met
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153 385                   390                   395                   400
155 Leu Met Asn Arg Lys Phe Ser Glu Glu Ala Ala Thr Trp Met Gln Glu
156                   405                   410                   415
158 Gln Arg Ala Thr Tyr Val Lys Ile Leu Ser Asn
159                   420                   425
162 <210> SEQ ID NO: 3
163 <211> LENGTH: 1287
164 <212> TYPE: DNA
165 <213> ORGANISM: Escherichia coli
167 <400> SEQUENCE: 3
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171 gcccccccagg tagtcgataa agtcgcagcc gtcgtcaata acggcgtcgt gctggaaagc   120
173 gacgttgatg gattaatgca gtcggtaaaa ctgaacgctg ctcaggcaag gcagcaactt   180
175 cctgatgacg cgacgctgcg ccaccaaatc atggaacgtt tgatcatgga tcaaatcatt   240
177 ctgcagatgg ggcagaaaat gggagtgaaa atctccgatg agcagctgga tcaggcgatt   300
179 gctaacatcg cgaaacagaa caacatgacg ctggatcaga tgcgcagccg tctggcttac   360
181 gatggactga actacaacac ctatcgtaac cagatccgca aagagatgat tatctctgaa   420
183 gtgcgtaaca cgaggtgcgc tcgtcgcatc accatcctgc cgcaggaagt cgaatccctg   480
185 gcgcagcagg tgggtaacca aaacgacgcc agcactgagc tgaacctgag ccacatcctg   540
187 atcccgctgc cggaaaaccc gacctctgat caggtgaacg aagcggaaag ccaggcgcgc   600
189 gccattgtcg atcaggcgcg taacggcgct gatttcggta agctggcgat tgctcattct   660
191 gccgaccagc aggcgctgaa cggcggccag atgggctggg ccgtattca ggagttgccc    720
193 gggatcttcg cccaggcatt aagcaccgcg aagaaaggcg acattgttgg cccgattcgt   780
195 tccggcgttg gcttccatat tctgaaagtt aacgacctgc gcggcgaaag caaaaatatc   840
197 tcggtgaccg aagttcatgc tcgccatatt ctgctgaaac cgtcgccgat catgactgac   900
199 gaacaggccc gtgtgaaact ggaacagatt gctgctgata tcgagagtgg taaaacgact   960
201 tttgctgccg caacgaaaga gttctctcag gatccagtct ctgctaacca gggcggcgat  1020
203 ctcggctggg ctacaccaga tattttcgat ccggccttcc gtgacgccct gactcgcctg  1080
205 aacaaaggtc aaatgagtgc accggttcac tcttcattcg gctggcattt aatcgaactg  1140
207 ctggataccc gtaatgtcga taaaaccgac gctgcgcaga aagatcgtgc ataccgcatg  1200
209 ctgatgaacc gtaagttctc ggaagaagca gcaagctgga tgcaggaaca acgtgccagc  1260
211 gcctacgtta aaatcctgag caactaa                                      1287
214 <210> SEQ ID NO: 4
215 <211> LENGTH: 428
216 <212> TYPE: PRT
217 <213> ORGANISM: Escherichia coli
219 <400> SEQUENCE: 4
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222  1               5                   10                  15
224 Thr Ser Phe Ala Ala Pro Gln Val Val Asp Lys Val Ala Ala Val Val
225              20                  25                  30
227 Asn Asn Gly Val Val Leu Glu Ser Asp Val Asp Gly Leu Met Gln Ser
228          35                  40                  45
230 Val Lys Leu Asn Ala Ala Gln Ala Arg Gln Gln Leu Pro Asp Asp Ala
231      50                  55                  60
233 Thr Leu Arg His Gln Ile Met Glu Arg Leu Ile Met Asp Gln Ile Ile
234 65                  70                  75                  80
236 Leu Gln Met Gly Gln Lys Met Gly Val Lys Ile Ser Asp Glu Gln Leu
237              85                  90                  95
```

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```
239 Asp Gln Ala Ile Ala Asn Ile Ala Lys Gln Asn Asn Met Thr Leu Asp
240          100              105              110
242 Gln Met Arg Ser Arg Leu Ala Tyr Asp Gly Leu Asn Tyr Asn Thr Tyr
243      115              120              125
245 Arg Asn Gln Ile Arg Lys Glu Met Ile Ile Ser Glu Val Arg Asn Asn
246      130              135              140
248 Glu Val Arg Arg Arg Ile Thr Ile Leu Pro Gln Glu Val Glu Ser Leu
249 145              150              155              160
251 Ala Gln Gln Val Gly Asn Gln Asn Asp Ala Ser Thr Glu Leu Asn Leu
252              165              170              175
254 Ser His Ile Leu Ile Pro Leu Pro Glu Asn Pro Thr Ser Asp Gln Val
255          180              185              190
257 Asn Glu Ala Glu Ser Gln Ala Arg Ala Ile Val Asp Gln Ala Arg Asn
258      195              200              205
260 Gly Ala Asp Phe Gly Lys Leu Ala Ile Ala His Ser Ala Asp Gln Gln
261      210              215              220
263 Ala Leu Asn Gly Gly Gln Met Gly Trp Gly Arg Ile Gln Glu Leu Pro
264 225              230              235              240
266 Gly Ile Phe Ala Gln Ala Leu Ser Thr Ala Lys Lys Gly Asp Ile Val
267              245              250              255
269 Gly Pro Ile Arg Ser Gly Val Gly Phe His Ile Leu Lys Val Asn Asp
270              260              265              270
272 Leu Arg Gly Glu Ser Lys Asn Ile Ser Val Thr Glu Val His Ala Arg
273          275              280              285
275 His Ile Leu Leu Lys Pro Ser Pro Ile Met Thr Asp Glu Gln Ala Arg
276      290              295              300
278 Val Lys Leu Glu Gln Ile Ala Ala Asp Ile Glu Ser Gly Lys Thr Thr
279 305              310              315              320
281 Phe Ala Ala Ala Thr Lys Glu Phe Ser Gln Asp Pro Val Ser Ala Asn
282              325              330              335
284 Gln Gly Gly Asp Leu Gly Trp Ala Thr Pro Asp Ile Phe Asp Pro Ala
285              340              345              350
287 Phe Arg Asp Ala Leu Thr Arg Leu Asn Lys Gly Gln Met Ser Ala Pro
288          355              360              365
290 Val His Ser Ser Phe Gly Trp His Leu Ile Glu Leu Leu Asp Thr Arg
291      370              375              380
293 Asn Val Asp Lys Thr Asp Ala Ala Gln Lys Asp Arg Ala Tyr Arg Met
294 385              390              395              400
296 Leu Met Asn Arg Lys Phe Ser Glu Glu Ala Ala Ser Trp Met Gln Glu
297              405              410              415
299 Gln Arg Ala Ser Ala Tyr Val Lys Ile Leu Ser Asn
300              420              425
```

VERIFICATION SUMMARY   DATE: 04/29/2002
PATENT APPLICATION: **US/09/591,447D**   TIME: 16:41:16

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Output Set: **N:\CRF3\04292002\I591447D.raw**